

SEQUENCE LISTING

<110> Novartis AG
 <120> ANTIBODY (11C7) ANTI NOGO A AND ITS PHARMACEUTICAL USE
 <130> 4-32761P1/UNZ
 <140> US/10/538,201
 <141> 2006-03-08
 <150> PCT/EP03/13960
 <151> 2003-12-09
 <150> UK 0228832.2
 <151> 2002-10-12
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 <170> PatentIn version 3.5
 <210> 1
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 <213> Rattus norvegicus

 <220>
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 <222> (1)..(18)
 <223> rat NogoA_623-640
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 Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu
 1 5 10 15

 Glu Ala

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 <213> Mus musculus

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 <222> (1)..(221)
 <223> Variable part of Heavy Chain of 11C7 with leader sequence
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 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
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 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
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 Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
 35 40 45

Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110

Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
130 135 140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
195 200 205

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
210 215 220

<210> 3
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<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)..(238)
<223> Light Chain of 11C7 with leader sequence

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Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile
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Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
 35 40 45
 Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
 50 55 60
 Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
 65 70 75 80
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 85 90 95
 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
 100 105 110
 Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
 115 120 125
 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
 130 135 140
 Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
 145 150 155 160
 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
 165 170 175
 Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
 180 185 190
 Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
 195 200 205
 Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
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 Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys
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<220>
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 <222> (1)..(3579)
 <223> Human NogoA

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tta aca gag ttt tca gaa tta gaa tac tca gaa atg gga tca tcg ttc Leu Thr 290 Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met 300 Gly Ser Ser Phe	912
agt gtc tct cca aaa gca gaa tct gcc gta ata gta gca aat cct agg Ser Val Ser Pro Lys Ala 310 Glu Ser Ala Val Ile Val Ala Asn Pro Arg 320	960
gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt Glu Glu Ile Ile Val 325 Lys Asn Lys Asp Glu Glu Glu Lys Leu Val 335 Ser	1008
aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa Asn Asn Ile 340 His Asn Gln 345 Glu Leu Pro Thr Ala Leu Thr Lys	1056
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gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag Ala Asp Phe Lys Pro Phe 390 Glu Arg Val Trp Glu Val Lys Asp Ser Lys 400	1200
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cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa Pro Leu Leu Gly Asp 485 Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys 495	1488
ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc Ile Glu Glu Lys 500 Lys Ala Gln Ile Val 505 Thr Thr Glu Lys Asn Thr Ser Thr	1536
aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat	1584

Lys	Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala	Ala	Gln	Asp	Ser	Glu	Thr	Asp	
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tat	gtc	aca	aca	gat	aat	tta	aca	aag	gtg	act	gag	gaa	gtc	gtg	gca	1632
Tyr	Val	Thr	Thr	Asp	Asn	Leu	Thr	Lys	Val	Thr	Glu	Glu	Val	Val	Ala	
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aac	atg	cct	gaa	ggc	ctg	act	cca	gat	tta	gta	cag	gaa	gca	tgt	gaa	1680
Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	
545					550					555					560	
agt	gaa	ttg	aat	gaa	gtt	act	ggg	aca	aag	att	gct	tat	gaa	aca	aaa	1728
Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	
				565					570					575		
atg	gac	ttg	gtt	caa	aca	tca	gaa	gtt	atg	caa	gag	tca	ctc	tat	cct	1776
Met	Asp	Leu	Val	Gln	Thr	Ser	Glu	Val	Met	Gln	Glu	Ser	Leu	Tyr	Pro	
			580					585					590			
gca	gca	cag	ctt	tgc	cca	tca	ttt	gaa	gag	tca	gaa	gct	act	cct	tca	1824
Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	Ser	Glu	Ala	Thr	Pro	Ser	
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cca	gtt	ttg	cct	gac	att	gtt	atg	gaa	gca	cca	ttg	aat	tct	gca	gtt	1872
Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu	Ala	Pro	Leu	Asn	Ser	Ala	Val	
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cct	agt	gct	ggc	gct	tcc	gtg	ata	cag	ccc	agc	tca	cca	tta	gaa		1920
Pro	Ser	Ala	Gly	Ala	Ser	Val	Ile	Gln	Pro	Ser	Ser	Ser	Pro	Leu	Glu	
625					630					635				640		
gct	tct	tca	gtt	aat	tat	gaa	agc	ata	aaa	cat	gag	cct	gaa	aac	ccc	1968
Ala	Ser	Ser	Val	Asn	Tyr	Glu	Ser	Ile	Lys	His	Glu	Pro	Glu	Asn	Pro	
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ata	aag	gaa	gaa	att	aaa	gag	cct	gaa	aat	att	aat	gca	gct	ctt	caa	2064
Ile	Lys	Glu	Glu	Ile	Lys	Glu	Pro	Glu	Asn	Ile	Asn	Ala	Ala	Leu	Gln	
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gaa	aca	gaa	gct	cct	tat	ata	tct	att	gca	tgt	gat	tta	att	aaa	gaa	2112
Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	
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aca	aag	ctt	tct	gct	gaa	cca	gct	ccg	gat	ttc	tct	gat	tat	tca	gaa	2160
Thr	Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro	Asp	Phe	Ser	Asp	Tyr	Ser	Glu	
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Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro	Asp	His	Ser	Glu	Leu	Val	Glu	
				725					730					735		
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Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	
			740					745					750			
ata	cct	gac	gtt	cca	caa	aaa	caa	gat	gaa	act	gtg	atg	ctt	gtg	aaa	2304
Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp	Glu	Thr	Val	Met	Leu	Val	Lys	
		755					760					765				
gaa	agt	ctc	act	gag	act	tca	ttt	gag	tca	atg	ata	gaa	tat	gaa	aat	2352
Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu	Ser	Met	Ile	Glu	Tyr	Glu	Asn	

770	775	780	
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gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro 805 810 815			2448
gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met 820 825 830			2496
gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct Glu Glu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser 835 840 845			2544
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att gaa att ata gat gag ttc cct aca ttg atc agt tct aaa act gat Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp 865 870 875 880			2640
tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His 885 890 895			2688
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tct gct ata ttt tca gca gag ctg agt aaa act tca gtt gtt gac ctc Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu 995 1000 1005			3024
ctg tac tgg aga gac att aag aag act gga gtg gtg ttt ggt gcc Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala 1010 1015 1020			3069
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gta aca gcc tac att gcc ttg gcc ctg ctg tct gtg acc atc agc	3159
Val Thr Ala Tyr Ile Ala Leu Val Val Thr Ile Ser	
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Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp	
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gaa ggc cac cca ttc agg gca tat ctg gaa tct gaa gtt gct ata	3249
Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile	
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tct gag gag ttg gtt cag aag tac agt aat tct gct ctt ggt cat	3294
Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His	
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gtg aac tgc acg ata aag gaa ctg agg cgc ctg ttc tta gtt gat	3339
Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp	
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gat tta gtt gat tct ctg aag ttt gca gtg ttg atg tgg gta ttt	3384
Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe	
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acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg	3429
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu	
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gct ctg att tca ctg ttc agt gtt cct gtt att tat gaa cgg cat	3474
Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His	
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cag gca cag ata gat cat tat cta gga ctt gca aat aag aat gtt	3519
Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val	
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aaa gat gct atg gct aaa atc caa gca aaa atc cct gga ttg aag	3564
Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys	
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cgc aaa gct gaa tga aaacgcccaa aataattagt aggagttcat ctttaaagg	3619
Arg Lys Ala Glu	
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agtttcacag atcgttggtta gatctttatt tttagccatg cactgttggtg agggaaaatt	3739
acctgtcttg actgccatgt gttcatcatc ttaagtattg taagctgcta tgataggatt	3799
taaacggtaa tcatatcttt ttctatctg aggcactggt ggaataaaaa acctgtatat	3859
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Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
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Asp Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
 35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
 50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
 65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
 85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
 100 105 110

Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
 115 120 125

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
 130 135 140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
 145 150 155 160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
 165 170 175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
 180 185 190

Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp
 195 200 205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe
 210 215 220

Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
 225 230 235 240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser
 245 250 255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
 260 265 270

Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp
 275 280 285

Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe
 290 295 300

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg
 305 310 315 320

Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser
 325 330 335

Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys
 340 345 350

Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser
 355 360 365

Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
 370 375 380

Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys
 385 390 395 400

Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu
 405 410 415

Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr
 420 425 430

Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro
 435 440 445

Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys
 450 455 460

Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe
 465 470 475 480

Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
 485 490 495

Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr
 500 505 510

Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp
 515 520 525

Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala
 530 535 540

Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
 545 550 555 560

Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys
 565 570 575

Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
 580 585 590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
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Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
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Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
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Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
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Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
 660 665 670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
 675 680 685

Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
 690 695 700

Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu
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Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
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Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
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Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
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Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn
 770 775 780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu

785		790		795		800
Glu Ser Phe Lys	Leu Ser Leu Asp Asn Thr	Lys Asp Thr Leu Leu Pro				
	805		810		815	
Asp Glu Val Ser Thr Leu Ser Lys	Lys Glu Lys Ile Pro Leu Gln Met					
	820		825		830	
Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp	Leu Phe Ile Ser					
	835		840		845	
Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro						
	850		855		860	
Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp						
	865		870		875	
Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His						
	885		890		895	
Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys						
	900		905		910	
Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val						
	915		920		925	
Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala						
	930		935		940	
Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr						
	945		950		955	
Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu						
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Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro						
	980		985		990	
Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu						
	995		1000		1005	
Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala						
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Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser						
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Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser						
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Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp
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Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile
1070 1075 1080

Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His
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Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp
1100 1105 1110

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
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Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu
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Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
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Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val
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Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys
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Arg Lys Ala Glu
1190

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<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Human NogoA_623-640

<400> 6

Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu
1 5 10 15

Glu Ala

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35 40 45

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His
50 55 60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu
65 70 75 80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys
85 90 95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr
100 105 110

Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly
210 215 220

Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe
 225 230 235 240
 Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser
 245 250 255
 Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg
 260 265 270
 Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu
 275 280 285
 Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu
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 Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val
 305 310 315 320
 Thr Glu Lys Asn Thr Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala
 325 330 335
 Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys
 340 345 350
 Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp
 355 360 365
 Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr
 370 375 380
 Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val
 385 390 395 400
 Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu
 405 410 415
 Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
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 Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln
 435 440 445
 Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile
 450 455 460
 Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val
 465 470 475 480

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu
 485 490 495

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
 500 505 510

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro
 515 520 525

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro
 530 535 540

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val
 545 550 555 560

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp
 565 570 575

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu
 580 585 590

Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro
 595 600 605

Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn
 610 615 620

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys
 625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser
 645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu
 660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr
 675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr
 690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp
 705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu
 725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp
740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr
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Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser
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Lys Thr Ser

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<211> 10
<212> PRT
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<220>
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<223> hypervariable part of heavy chain of 11C7

<400> 8

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<210> 9
<211> 17
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(17)
<223> hypervariable part of heavy chain of 11C7

<400> 9

Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys
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Asp

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<223> hypervariable part of heavy chain of 11C7

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<212> PRT

<213> Mus musculus

<220>

<221> BINDING

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<223> hypervariable part of light chain of 11C7

<400> 11

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn
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<210> 12

<211> 7

<212> PRT

<213> Mus musculus

<220>

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<223> hypervariable part of light chain of 11C7

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<210> 13

<211> 9

<212> PRT

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<220>

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<220>
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 <212> DNA
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<220>
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 <222> (1)..(51)
 <223> DNA-CDR2-11C7

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<210> 16
 <211> 27
 <212> DNA
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<220>
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 <223> DNA-CDR3-11C7

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<210> 17
 <211> 48
 <212> DNA
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<220>
 <221> misc_binding
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 <223> DNA-CDR'1-11C7

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<210> 20
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<220>
 <221> CDS
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 <223> leader sequence for heavy chain of 11C7

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 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
 1 5 10 15
 cag tgt
 Gln Cys 54

<210> 21
 <211> 18
 <212> PRT
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<400> 21
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 1 5 10 15
 Gln Cys

<210> 22
 <211> 57
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(57)
 <223> leader sequence for 11C7-light chain

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 Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
 1 5 10 15
 acc agc ggt
 Thr Ser Gly 57

<210> 23
 <211> 19
 <212> PRT
 <213> Mus musculus

<400> 23
 Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
 1 5 10 15
 Thr Ser Gly

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 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
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 <223> human Nig-D20

<400> 24
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 20 25 30
 Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
 35 40 45
 Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
 50 55 60
 Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
 65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
85 90 95

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
100 105 110

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile
115 120 125

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
130 135 140

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
145 150 155 160

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
165 170 175

Pro Val Asp Leu Phe
180

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<211> 3492
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(3492)
<223> rat NogoA

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1 5 10		
ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc		96
Pro Pro Arg Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro		
20 25 30		
gag gac gag gag gac gag gag gag gag gac gag gag gag gac gac		144
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Asp Asp		
35 40 45		
gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg		192
Glu Asp Leu Glu Glu Glu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly		
50 55 60		
ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg ctg ctg gac		240
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp		
65 70 75 80		
ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg ctg ccg gcc		288
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala		
85 90 95		
gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc		336

Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Glu	Arg	Ser	Pro	
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gcg	gcg	ccc	gcg	cca	tcc	ctg	ccg	ccc	gct	gcc	gca	gtc	ctg	ccc	tcc	384
Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser	
			115				120					125				
aag	ctc	cca	gag	gac	gac	gag	cct	ccg	gcg	agg	ccc	ccg	cct	ccg	ccg	432
Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	
			130			135					140					
cca	gcc	ggc	gcg	agc	ccc	ctg	gcg	gag	ccc	gcc	gcg	ccc	cct	tcc	acg	480
Pro	Ala	Gly	Ala	Ser	Pro	Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr	
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ccg	gcc	gcg	ccc	aag	cgc	agg	ggc	tcc	ggc	tca	gtg	gat	gag	acc	ctt	528
Pro	Ala	Ala	Pro	Lys	Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	
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ttt	gct	ctt	cct	gct	gca	tct	gag	cct	gtg	ata	ccc	tcc	tct	gca	gaa	576
Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu	
			180					185					190			
aaa	att	atg	gat	ttg	atg	gag	cag	cca	ggt	aac	act	gtt	tcg	tct	ggc	624
Lys	Ile	Met	Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly	
			195				200					205				
caa	gag	gat	ttc	cca	tct	gtc	ctg	ctt	gaa	act	gct	gcc	tct	ctt	cct	672
Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	
			210			215					220					
tct	cta	tct	cct	ctc	tca	act	gtt	tct	ttt	aaa	gaa	cat	gga	tac	ctt	720
Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu	
				230						235				240		
ggt	aac	tta	tca	gca	gtg	tca	tcc	tca	gaa	gga	aca	att	gaa	gaa	act	768
Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Val	Thr	
				245					250					255		
tta	aat	gaa	gct	tct	aaa	gag	ttg	cca	gag	agg	gca	aca	aat	cca	ttt	816
Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Pro	Pro	Phe	
			260					265					270			
gta	aat	aga	gat	tta	gca	gaa	ttt	tca	gaa	tta	gaa	tat	tca	gaa	atg	864
Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	
			275				280					285				
gga	tca	tct	ttt	aaa	ggc	tcc	cca	aaa	gga	gag	tca	gcc	ata	tta	gta	912
Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val	
			290			295					300					
gaa	aac	act	aag	gaa	gaa	gta	att	gtg	agg	agt	aaa	gac	aaa	gag	gat	960
Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp	
			305		310				315					320		
tta	gtt	tgt	agt	gca	gcc	ctt	cac	agt	cca	caa	gaa	tca	cct	gtg	ggc	1008
Leu	Val	Cys	Ser	Ala	Ala	Leu	His	Ser	Pro	Gln	Glu	Ser	Pro	Val	Gly	
				325					330					335		
aaa	gaa	gac	aga	gtt	gtg	tct	cca	gaa	aag	aca	atg	gac	att	ttt	aat	1056
Lys	Glu	Asp	Arg	Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn	
			340					345				350				
gaa	atg	cag	atg	tca	gta	gta	gca	cct	gtg	agg	gaa	gag	tat	gca	gac	1104
Glu	Met	Gln	Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp	

355				360				365								
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aga Arg	aaa Lys	tgç Cys	ttg Leu	gaa Glu 405	gat Asp	agc Ser	ctg Leu	gag Glu	caa Gln 410	aaa Lys	agt Ser	ctt Leu	ggg Gly	aag Lys 415	gat Asp	1248
agt Ser	gaa Glu	ggc Gly	aga Arg 420	aat Asn	gag Glu	gat Asp	gct Ala	tct Ser 425	ttc Phe	ccc Pro	agt Ser	acc Thr	cca Pro 430	gaa Glu	cct Pro	1296
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caa Gln	att Ile	ata Ile	aca Thr	gag Glu 485	aag Lys	act Thr	agc Ser	ccc Pro	aaa Lys 490	acg Thr	tca Ser	aat Asn	cct Pro	ttc Phe 495	ctt Leu	1488
gta Val	gca Ala	gta Val 500	gln Gln	gat Asp	tct Ser	gag Glu	gca Ala	gat Asp 505	tat Tyr	ggt Val	aca Thr	aca Thr	gat Asp 510	acc Thr	tta Leu	1536
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cca Pro	gat Asp 530	tta Leu	gtt Val	cag Gln	gaa Glu	gca Ala 535	tgt Cys	gaa Glu	agt Ser	gaa Glu	ctg Leu 540	aat Asn	gaa Glu	gcc Ala	aca Thr	1632
ggg Gly 545	aca Thr	aag Lys	att Ile	gct Ala	tat Tyr 550	gaa Glu	aca Thr	aaa Lys	gtg Val	gac Asp 555	ttg Leu	gtc Val	caa Gln	aca Thr	tca Ser 560	1680
gaa Glu	gct Ala	ata Ile	caa Gln	gaa Glu 565	tca Ser	ctt Leu	tac Tyr	ccc Pro	aca Thr 570	gca Ala	cag Gln	ctt Leu	tgç Cys	cca Pro 575	tca Ser	1728
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gtg Val	cag Gln 610	ccc Pro	agt Ser	gta Val	tcc Ser	cca Pro 615	ctg Leu	gaa Glu	gca Ala	cct Pro	cct Pro 620	cca Pro	gtt Val	agt Ser	tat Tyr	1872

gac Asp 625	agt Ser	ata Ile	aag Lys	ctt Leu	gag Glu 630	cct Pro	gaa Glu	aac Asn	ccc Pro	cca Pro 635	cca Pro	tat Tyr	gaa Glu	gaa Glu 640	gcc Ala	1920
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cct Pro	gaa Glu	agt Ser	ttt Phe 660	aat Asn	gca Ala	gct Ala	gtt Val	cag Gln 665	gaa Glu	aca Thr	gaa Glu	gct Ala	cct Pro 670	tat Tyr	ata Ile	2016
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agt Ser	cca Pro 690	gat Asp	ttc Phe	tct Ser	aat Asn	tat Tyr 695	tca Ser	gaa Glu	ata Ile	gca Ala	aaa Lys 700	ttc Phe	gag Glu	aag Lys	tcg Ser	2112
gtg Val 705	ccc Pro	gaa Glu	cac His	gct Ala	gag Glu 710	cta Leu	gtg Val	gag Glu	gat Asp	tcc Ser 715	tca Ser	cct Pro	gaa Glu	tct Ser	gaa Glu 720	2160
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aca Thr 785	aaa Lys	gat Asp	gct Ala	gca Ala	tct Ser 790	aat Asn	gac Asp	att Ile	cca Pro	aca Thr 795	ttg Leu	acc Thr	aaa Lys	aag Lys	gag Glu 800	2400
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gat Asp	gac Asp	tta Leu	ctt Leu 820	tct Ser	tct Ser	aag Lys	gaa Glu	gac Asp 825	aaa Lys	ata Ile	aaa Lys	gaa Glu	agt Ser 830	gaa Glu	aca Thr	2496
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agt gta acg gcc tac att gcc ttg gcc ctg ctg tcg gtg act atc Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile 1010 1015 1020	3069
agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa tca Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser 1025 1030 1035	3114
gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala 1040 1045 1050	3159
ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly 1055 1060 1065	3204
cat gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val 1070 1075 1080	3249
gat gat tta gtt gat tcc ctg aag ttt gca gtg ttg atg tgg gtg Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val 1085 1090 1095	3294
ttt act tat gtt ggt gcc ttg ttc aat ggt ctg aca cta ctg att Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile 1100 1105 1110	3339
tta gct ctg atc tca ctg ttc agt att cct gtt att tat gaa cgg Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg 1115 1120 1125	3384
cat cag gtg cag ata gat cat tat cta gga ctt gca aac aag agt	3429

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser
 1130 1135 1140

gtt aag gat gcc atg gcc aaa atc caa gca aaa atc cct gga ttg 3474
 Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
 1145 1150 1155

aag cgc aaa gca gat tga 3492
 Lys Arg Lys Ala Asp
 1160

<210> 26
 <211> 1163
 <212> PRT
 <213> Rattus norvegicus

<400> 26

Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser
 1 5 10 15

Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
 20 25 30

Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
 35 40 45

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
 50 55 60

Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
 65 70 75 80

Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
 85 90 95

Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
 100 105 110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
 115 120 125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
 130 135 140

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
 145 150 155 160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
 165 170 175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
 180 185 190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
 195 200 205
 Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
 210 215 220
 Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
 225 230 235 240
 Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
 245 250 255
 Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
 260 265 270
 Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
 275 280 285
 Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
 290 295 300
 Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
 305 310 315 320
 Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
 325 330 335
 Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
 340 345 350
 Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
 355 360 365
 Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
 370 375 380
 Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
 385 390 395 400
 Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
 405 410 415
 Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
 420 425 430
 Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
 435 440 445

Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
 450 455 460

Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
 465 470 475 480

Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
 485 490 495

Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
 500 505 510

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
 515 520 525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
 530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
 545 550 555 560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
 565 570 575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
 580 585 590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
 595 600 605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
 610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
 625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
 645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
 660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
 675 680 685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
 690 695 700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
 705 710 715 720
 Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
 725 730 735
 Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
 740 745 750
 Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
 755 760 765
 Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
 770 775 780
 Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
 785 790 795 800
 Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
 805 810 815
 Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
 820 825 830
 Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
 835 840 845
 Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
 850 855 860
 Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
 865 870 875 880
 Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
 885 890 895
 Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
 900 905 910
 Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
 915 920 925
 Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
 930 935 940
 Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
 945 950 955 960
 Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val

965

970

975

Val Asp Leu ^{Leu} Tyr Trp Arg Asp ^{Ile} Lys Lys Thr Gly Val Val Phe
 980 985 990

Gly Ala Ser Leu Phe Leu Leu ^{Leu} Ser Leu Thr Val ^{Phe} Ser Ile Val
 995 1000 1005

Ser Val Thr Ala Tyr Ile ^{Ala} Leu Ala Leu Leu Ser Val Thr Ile
 1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala ^{Ile} Gln Lys Ser
 1025 1030 1035

Asp Glu Gly His Pro Phe ^{Arg} Ala Tyr Leu Glu Ser Glu Val Ala
 1040 1045 1050

Ile Ser Glu Glu Leu Val ^{Gln} Lys Tyr Ser Asn Ser Ala Leu Gly
 1055 1060 1065

His Val Asn Ser Thr Ile ^{Lys} Glu Leu Arg Arg ^{Leu} Phe Leu Val
 1070 1075 1080

Asp Asp Leu Val Asp Ser ^{Leu} Lys Phe Ala Val ^{Leu} Met Trp Val
 1085 1090 1095

Phe Thr Tyr Val Gly Ala ^{Leu} Phe Asn Gly Leu Thr Leu Leu Ile
 1100 1105 1110

Leu Ala Leu Ile Ser Leu ^{Phe} Ser Ile Pro Val ^{Ile} Tyr Glu Arg
 1115 1120 1125

His Gln Val Gln Ile Asp ^{His} Tyr Leu Gly Leu ^{Ala} Asn Lys Ser
 1130 1135 1140

Val Lys Asp Ala Met Ala ^{Lys} Ile Gln Ala Lys ^{Ile} Pro Gly Leu
 1145 1150 1155

Lys Arg Lys Ala Asp
 1160

<210> 27
 <211> 25
 <212> PRT
 <213> Rattus norvegicus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> rat PEP4

<400> 27

Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn
1 5 10 15

Ser Thr Ile Lys Glu Leu Arg Arg Leu
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro
1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-2F

<220>

<221> primer_bind

<222> (1)..(25)

<223> CA-NA-2F primer

<400> 29

aagcaccatt gaattctgca gtccc

25

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

<220>

<221> primer_bind

<222> (1)..(28)

<400> 30
aactgcagta ctgagctcct ccatctgc 28

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> forward 5'

<220>
<221> primer_bind
<222> (1)..(33)
<223> forward primer

<400> 31
gtcgcggatc catggagacc ctttttgctc ttc 33

<210> 32
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse 5'

<220>
<221> primer_bind
<222> (1)..(27)
<223> reverse primer

<400> 32
gttctcgagt tatgaagttt tactcag 27

<210> 33
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> forward 5'-1

<220>
<221> primer_bind
<222> (1)..(29)
<223> primer

<400> 33
gtcgcgatcc atggatttga aggagcagc 29

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> reverse 5'-1

 <220>
 <221> primer_bind
 <222> (1)..(28)
 <223> primer

 <400> 34
 gtttctcgag tgaagtttta ttcagctc 28

 <210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5' primer

 <220>
 <221> primer_bind
 <222> (1)..(20)
 <223> primer

 <400> 35
 tccaccccg cgcgccccaa 20

 <210> 36
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5' primer 2

 <220>
 <221> primer_bind
 <222> (1)..(22)
 <223> primer

 <400> 36
 aatgatgggc aaagctgtgc tg 22

 <210> 37
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' primer

 <220>
 <221> primer_bind
 <222> (1)..(24)
 <223> primer

 <400> 37
 ggtacaaaga ttgcttatga aaca 24

<210> 38
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer 2

<220>
<221> primer_bind
<222> (1)..(22)
<223> primer

<400> 38
agcagggccca aggcaatgta gg

22

<210> 39
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'-VL leader

<220>
<221> primer_bind
<222> (1)..(28)
<223> primer

<400> 39
aatatgagtc ctgcccagtt cctgtttc

28

<210> 40
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> 3'-Ck

<220>
<221> primer_bind
<222> (1)..(32)
<223> primer

<400> 40
ttaggaattc ctaacactct cccctgttga ag

32

<210> 41
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'-VH leader

<220>

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<221> primer_bind
<222> (1)..(31)
<223> primer

<400> 41
aatatggatt ttgggctgat tttttttatt g 31

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 3'-CH hinge

<220>
<221> primer_bind
<222> (1)..(24)
<223> primer

<400> 42
aattgggcaa cggtgcaggt gacg 24

<210> 43
<211> 663
<212> DNA
<213> Mus musculus

<220>
<221> misc_binding
<222> (1)..(663)
<223> DNA variable part of heavy chain 11c7

<400> 43
atggattttg ggctgatttt ttttattgtt ggtcttttaa aaggggtcca ggtgaggtg 60
aagcttctcg agtctggagg tggcctgggt cagcctggag gatccctgaa actctcctgt 120
gtagtctcag gattcgtatt tagaagaaat tggatgagtt gggtcaggca ggctcctggg 180
aaagggctag aatggattgg agaaattaat ccagatagca gtaagataaa ctatacgcca 240
tctctaaagg ataaattcat catctccaga gacaatgcca agaatacgtc gtacctgcaa 300
gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg 360
tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctctcagc caaaacgaca 420
cccccatctg tctatccact ggccctgga tctgtgtccc aaactaacct catggtgacc 480
ctgggatgcc tgggtcaaggg ctatttcctt gagccagtga cagtgcctgt gaactctgga 540
tccctgtcca gcggtgtgca caccctccca gctgtcctgc agtctgacct ctacactctg 600
agcagctcag tgactgtccc ctccagcacc tggcccgagc agaccgtcac ctgcaacgtt 660
gcc 663

<210> 44
<211> 717

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<212> DNA
<213> Mus musculus

<220>
<221> misc_binding
<222> (1)..(717)
<223> variable part of light chain of 11C7

<400> 44
atgagtcctg cccagttcct gtttctgtta gtgctctgga ttcgggaaac cagcgggtgat 60
gttctgttga cccagatccc tctcactttg tcgataacca ttggacaacc agcctccatc 120
tcttgcaagt caagtcagag cctcttgcag agtgaatgaa agacatattt gaattgggtg 180
ttacagaggc caggccagtc tccaaagcgc ctaatctatc tgggtgtctaa actggactct 240
ggagtcctg acaggttcac tggcagtgga tcaggggcgg atttcacact gaaaatcagc 300
agagtggagg ctgaggattt gggactttat tattgctggc aaggtacaca ttttcctcag 360
acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420
atctccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 480
aacaacttct accccaaga catcaatgac aagtggaga ttgatggcag tgaacgacaa 540
aatggcgctc tgaacagttg gactgatcag gacagcaag acagcaccta cagcatgagc 600
agcaccctca cggtgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 660
actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag 717

<210> 45
<211> 239
<212> PRT
<213> Homo sapiens

<400> 45

Thr Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
35 40 45

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
85 90 95

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
100 105 110

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
115 120 125

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
130 135 140

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
165 170 175

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
180 185 190

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
195 200 205

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys
210 215 220

Gln Asp Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr
225 230 235

<210> 46
<211> 239
<212> PRT
<213> Pan paniscus

<400> 46

Gly Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
35 40 45

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Ala

85

90

95

Val Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
100 105 110

Ser Ile Ile His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
115 120 125

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
130 135 140

Pro Glu Ser Ile Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
165 170 175

Thr Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
180 185 190

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
195 200 205

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys
210 215 220

Gln Asp Glu Ala Val Met Leu Val Lys Glu Asn Leu Pro Glu Thr
225 230 235

<210> 47

<211> 239

<212> PRT

<213> Rattus norvegicus

<400> 47

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
35 40 45

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
85 90 95

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
100 105 110

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
115 120 125

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
130 135 140

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
165 170 175

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
180 185 190

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
195 200 205

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
210 215 220

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val
225 230 235

<210> 48
<211> 239
<212> PRT
<213> Mus musculus

<400> 48

Ser Lys Val Thr Glu Ala Val Val Ala Thr Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
35 40 45

Glu Ala Ile Gln Glu Ser Ile Tyr Pro Thr Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val

65		70		75		80
Met Glu Ala Pro	Leu Asn Ser Leu Leu	Pro Ser Thr Gly Ala	Ser Val			
	85	90	95			
Ala Gln Pro Ser	Ala Ser Pro Leu	Glu Val Pro Ser Pro	Val Ser Tyr			
	100	105	110			
Asp Gly Ile Lys	Leu Glu Pro	Glu Asn Pro Pro Pro	Tyr Glu Glu Ala			
	115	120	125			
Met Ser Val Ala	Leu Lys Thr Ser Asp Ser	Lys Glu Glu Ile Lys Glu				
	130	135	140			
Pro Glu Ser Phe	Asn Ala Ala Ala Gln Glu	Ala Glu Ala Pro Tyr Ile				
	145	150	155			160
Ser Ile Ala Cys	Asp Leu Ile Lys Glu Thr	Lys Leu Ser Thr Glu Pro				
	165	170	175			
Ser Pro Glu Phe	Ser Asn Tyr Ser Glu Ile Ala Lys Phe	Glu Lys Ser				
	180	185	190			
Val Pro Asp His	Cys Glu Leu Val Asp Asp Ser Ser	Pro Glu Ser Glu				
	195	200	205			
Pro Val Asp Leu	Phe Ser Asp Asp Ser Ile Pro Glu Val	Pro Gln Thr				
	210	215	220			
Gln Glu Glu Ala	Val Met Leu Met Lys Glu Ser Leu Thr Glu Val					
	225	230	235			